

SEQUENCE LISTING

<110> KITAMURA, Toshio

<120> Cytokine receptor-like proteins

<130> C1-102PCT

<140>

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<150> JP 1999-041936

<151> 1999-02-19

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 1278

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (59).. (1135)

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accggctcgg accgaaccag ctgtcaatca ctgcagcgtc cgcggccccg ccggcgac 58

atg gca tgg gca ctc gcg gtc atc ctc ctg cct cgg ctc ctt acg gcg 106

Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala

1

5

10

15

gca gcg gcg gcg gcg gcg gtg acg tca cgg ggt gat gtc aca gtc gtc 154

Ala Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val

20

25

30

tgc cat gac ctg gag acg gtg gag gtc acg tgg ggc tgc ggc ccc gac 202

Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp

35

40

45

cac cac ggc gcc aac ttg agc ctg gag ttc cgt tat ggt act ggc gcc 250

His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala

50

55

60

ctg caa ccc tgc ccg cga tat ttc ctg tcc ggc gct ggt gtc act tcc 298

Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser

65

70

75

80

ggg tgc atc ctc ccc gcg gcg agg gcg ggg ctg ctg gag ctg gca ctg 346

Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu

85

90

95

cgc gac gga ggc ggg gcc atg gtg ttt aag gct agg cag cgc gcg tcc 394

Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser

100

105

110

gcc tgg ctg aag ccc cgc cca cct tgg aat gtg acg ctg ctc tgg aca 442

Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr

115

120

125

cca gac ggg gac gtg act gtc tcc tgg cct gcc cac tcc tac ctg ggc 490

Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly

130

135

140

ctg gac tac gag gtg cag cac cgg gag agc aat gac gat gag gac gcc 538

Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala

145

150

155

160

tgg cag acg acc tca ggg ccc tgc tgt gac ttg aca gtg ggc ggg ctc 586

Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Leu

165

170

175

gac ccc gcg cgc tgc tat gac ttc cgg gtt cgg gcg tgc ccc cgg gcc 634

Asp Pro Ala Arg Cys Tyr Asp Phe Arg Val Arg Ala Ser Pro Arg Ala

180

185

190

gcg cac tat ggc ctg gag gcg cag cct agc gag tgg aca gcg gtg aca 682

Ala His Tyr Gly Leu Glu Ala Gln Pro Ser Glu Trp Thr Ala Val Thr

195

200

205

agg ctt tcc ggg gca gca tcc gcg gcc tcc tgt acc gca agc ccc gcc 730

Arg Leu Ser Gly Ala Ala Ser Ala Ala Ser Cys Thr Ala Ser Pro Ala

210

215

220

cca tcc ccg gcc ctg gcc ccg ccc ctc ctg ccc ctg ggc tgc ggc cta 778

Pro Ser Pro Ala Leu Ala Pro Pro Leu Leu Pro Leu Gly Cys Gly Leu

225

230

235

240

gca gcg ctg ctg aca ctg tcc ctg ctc ctg gcc gcc ctg agg ctt cgc 826

Ala Ala Leu Leu Thr Leu Ser Leu Leu Leu Ala Ala Leu Arg Leu Arg

245

250

255

agg gtg aaa gat gcg ctg ctg ccc tgc gtc cct gac ccc agc ggc tcc 874

Arg Val Lys Asp Ala Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser

260

265

270

ttc cct gga ctc ttt gag aag cat cac ggg aac ttc cag gcc tgg att 922

Phe Pro Gly Leu Phe Glu Lys His His Gly Asn Phe Gln Ala Trp Ile

275

280

285

gcg gac gcc cag gcc aca gcc ccg cca gcc agg acc gag gag gaa gat 970

Ala Asp Ala Gln Ala Thr Ala Pro Pro Ala Arg Thr Glu Glu Glu Asp

290

295

300

gac ctc atc cac ccc aag gct aag agg gtg gag ccc gag gac ggc acc 1018

Asp Leu Ile His Pro Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr

305

310

315

320

tcc ctc tgc acc gtg cca agg cca ccc agc ttc gag cca agg ggg ccg 1066

Ser Leu Cys Thr Val Pro Arg Pro Pro Ser Phe Glu Pro Arg Gly Pro

325

330

335

gga ggc ggg gcc atg gtg tca gtg ggc ggg gcc acg ttc atg gtg ggc 1114

Gly Gly Gly Ala Met Val Ser Val Gly Gly Ala Thr Phe Met Val Gly

340

345

350

gac agc ggc tac atg acc ctg tgaccttgaa gtcaactgcca gtctatactt 1165

Asp Ser Gly Tyr Met Thr Leu

355

caggctgagg tcacttcctg tctttaaata attcaaactc acaaatcctg tgccgtgtctg 1225

tatgcaaatg tggtcacgaa tattcaaata aaatgcaaat gctatgctaa aaa 1278

6/24

<211> 359

<212> PRT

<213> Mus musculus

<400> 2

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Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val

20 25 30

Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp

35 40 45

His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala

50 55 60

Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser

65 70 75 80

Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu

85 90 95

Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser

100 105 110

7/24

Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr

115

120

125

Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly

130

135

140

Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala

145

150

155

160

Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Leu

165

170

175

Asp Pro Ala Arg Cys Tyr Asp Phe Arg Val Arg Ala Ser Pro Arg Ala

180

185

190

Ala His Tyr Gly Leu Glu Ala Gln Pro Ser Glu Trp Thr Ala Val Thr

195

200

205

Arg Leu Ser Gly Ala Ala Ser Ala Ala Ser Cys Thr Ala Ser Pro Ala

210

215

220

Pro Ser Pro Ala Leu Ala Pro Pro Leu Leu Pro Leu Gly Cys Gly Leu

225

230

235

240

Ala Ala Leu Leu Thr Leu Ser Leu Leu Leu Ala Ala Leu Arg Leu Arg

245

250

255

8/24

Arg Val Lys Asp Ala Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser

260

265

270

Phe Pro Gly Leu Phe Glu Lys His His Gly Asn Phe Gln Ala Trp Ile

275

280

285

Ala Asp Ala Gln Ala Thr Ala Pro Pro Ala Arg Thr Glu Glu Glu Asp

290

295

300

Asp Leu Ile His Pro Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr

305

310

315

320

Ser Leu Cys Thr Val Pro Arg Pro Pro Ser Phe Glu Pro Arg Gly Pro

325

330

335

Gly Gly Gly Ala Met Val Ser Val Gly Gly Ala Thr Phe Met Val Gly

340

345

350

Asp Ser Gly Tyr Met Thr Leu

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(210) 3

(211) 804

(212) DNA

9/24

<213> Mus musculus

<220>

<221> CDS

<222> (98).. (661)

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tgtcaatcac tgcagcgtcc gcggccccgc cggcgac atg gca tgg gca ctc gcg 115

Met Ala Trp Ala Leu Ala

1

5

gtc atc ctc ctg cct cgg ctc ctt acg gcg gca gcg gcg gcg gcg gcg 163

Val Ile Leu Leu Pro Arg Leu Leu Thr Ala Ala Ala Ala Ala Ala Ala

10

15

20

gtg acg tca cgg ggt gat gtc aca gtc gtc tgc cat gac ctg gag acg 211

Val Thr Ser Arg Gly Asp Val Thr Val Val Cys His Asp Leu Glu Thr

25

30

35

gtg gag gtc acg tgg ggc tcg ggc ccc gac cac cac ggc gcc aac ttg 259

Val Glu Val Thr Trp Gly Ser Gly Pro Asp His His Gly Ala Asn Leu

40

45

50

age ctg gag ttc cgt tat ggt act ggc gcc ctg caa ccc tgc ccg cga 307

10/24

Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala Leu Gln Pro Cys Pro Arg

55

60

65

70

tat ttc ctg tcc ggc gct ggt gtc act tcc ggg tgc atc ctc ccc gcg 355

Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser Gly Cys Ile Leu Pro Ala

75

80

85

gcg agg gcg ggg ctg ctg gag ctg gca ctg cgc gac gga ggc ggg gcc 403

Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu Arg Asp Gly Gly Gly Ala

90

95

100

atg gtg ttt aag gct agg cag cgc gcg tcc gcc tgg ctg aag ccc cgc 451

Met Val Phe Lys Ala Arg Gln Arg Ala Ser Ala Trp Leu Lys Pro Arg

105

110

115

cca cct tgg aat gtg acg ctg ctc tgg aca cca gac ggg gac gtg act 499

Pro Pro Trp Asn Val Thr Leu Leu Trp Thr Pro Asp Gly Asp Val Thr

120

125

130

gtc tcc tgg cct gcc cac tcc tac ctg ggc ctg gac tac gag gtg cag 547

Val Ser Trp Pro Ala His Ser Tyr Leu Gly Leu Asp Tyr Glu Val Gln

135

140

145

150

cac cgg gag agc aat gac gat gag gac gcc tgg cag acg acc tca ggg 595

His Arg Glu Ser Asn Asp Asp Glu Asp Ala Trp Gln Thr Thr Ser Gly

155

160

165

11/24

ccc tgc tgt gac ttg aca gtg ggc ggg gcc acg ttc atg gtg ggc gac 643

Pro Cys Cys Asp Leu Thr Val Gly Gly Ala Thr Phe Met Val Gly Asp

170

175

180

agc ggc tac atg acc ctg tgaccttgaa gtcactgccca gtctatactt 691

Ser Gly Tyr Met Thr Leu

185

caggctgagg tcacttcttg tctttaaata attcaaactc acaaatcctg tgctgtctg 751

tatgcaaatg tggtcacgaa tattcaaata aaatgcaaatt gctatgctaa aaa 804

<210> 4

<211> 188

<212> PRT

<213> Mus musculus

<400> 4

Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala

1

5

10

15

Ala Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val

20

25

30

12/24

Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp

35

40

45

His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala

50

55

60

Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser

65

70

75

80

Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu

85

90

95

Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser

100

105

110

Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr

115

120

125

Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly

130

135

140

Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala

145

150

155

160

Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Ala

165

170

175

Thr Phe Met Val Gly Asp Ser Gly Tyr Met Thr Leu

180

185

<210> 5

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 5

gggggtggac catcctcta

19

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 6

cgcgagctg taaacggtag

20

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 7

ggtgatgtca cagtcgtctg ccatg

25

<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 8

acgggtccgca ggagtagcag taa

23

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 9

aaagaattcc cgcacctcct gcccttggc

30

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 10

gctggcggcc gcacctgcag gcgc

24

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 11

aaagaattcg ggggctgtat catggac

27

<210> 12

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 12

aaagaattcg ggggtccaggt cgctagg

27

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 13

ggtagggaat tccggaattt cctcgagatg

30

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 14

aaagaattcc caggcgggtct cggtaggcggt

30

<210> 15

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 15

aaagaattcg ttaacccgcc cctcctgccc ctgggg

36

<210> 16

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 16

aaagcggccg cctcgagcca ggcctggaag ttccc

35

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 17

aaactcgagc tgtaccagaa tgatggc

27

<210> 18

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 18

aaagcggccg ctcacttgtc agagcaagcc acatagct

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<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 19

aaagcggccg ctcagtcac agagcaagcc acatagct

38

<210> 20

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 20

aaagcggccg ctcagtcctt agagcaagcc acatagct

38

<210> 21

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

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aaagcggccg ctcagtaatc agagcaagcc acatagct

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<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 22

aaagaattcg ggggctgtat catggac

27

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 23

aaagttaacg ggggtccaggt cgctagg

27

<210> 24

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed peptide sequence

<400> 24

Asp Tyr Lys Asp Asp Asp Asp Lys

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<210> 25

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 25

agggaattcc ggaatttcct cgagatc

27

<210> 26

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence

<400> 26

aaagcggccg ctcacttgtc gtcacgtcc ttgtaatcca gggtcatgta gccgctgtc 59